UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/945,326	08/31/2001	Rachel Meyers	MPI00-344P1RM	2458

30405 7590 02/03/2006

MILLENNIUM PHARMACEUTICALS, INC.
40 Landsdowne Street
CAMBRIDGE, MA 02139

EXAMINER	
YU, MISOOK	
ART UNIT	**PAPER NUMBER**
1642	

DATE MAILED: 02/03/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/945,326	MEYERS ET AL.	
	Examiner	Art Unit	
	MISOOK YU, Ph.D.	1642	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *14 November 2005*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *64-72* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *64-72* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date 11/14/05
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

Claims 64-72 are pending and under consideration.

The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.

Claim Rejections - 35 USC § 101, Maintained

Claims 64-72 rejected under 35 U.S.C. 101 because the claimed invention is not supported by either a substantial asserted utility or a well established utility.

Claim 64-72 are interpreted as drawn to method of identifying a compound binding to SED ID NO:2 and also cytotoxic to cancer cells in vitro. The specification speculates that SEQ ID NO:2 might have utilities in making antibody, surrogate biomarkers, screening assays, chromosome mapping page, tissue typing, forensic biology, predictive medicine, diagnostic assay, prognostic assays, monitoring effects during clinical trials, methods of treatment, prophylactic methods, therapeutic methods, pharmacogenomics. These utilities are not considered to be specific and substantial because neither the specification nor any art of record teaches what the biological activities of SEQ ID NO:2 are, how they function, or a specific and well-established utility for SEQ ID NO:2 protein.

Applicant argues that the specification at pages 10-12, Fig. 2 teach that the instantly claimed SEQ ID NO: 2 is an acyl-coA dehydrogenase, and Zhang et al., (IDS, Biochem Biophys Res Commun., 2002 Oct 4;297(4):1033-42) at Fig. 5 teach that the protein (i.e. ACAD-9) identical to the instant SEQ ID NO: 2 has deydrogenase activity.

These arguments have been fully considered but found unpersuasive. As shown in Fig. 5, the recombinant ACAD-9 protein catalyzes oxidation of stearoyl-CoA (C18:0) and palmitoyl-CoA (C16:0). But the recombinant ACAD-9 has little effect on *n*-octanoyl-CoA (C8:0), *n*-butyryl-CoA (C4:0) or isovaleryl-CoA (C5:0). Here, Zhang et al., confirms the earlier Office's position using Voet reference, who teach that there are numerous dehydrogenases, each working on a specific substrate and generating a specific product, for example succinate dehyrogenase uses succinate as its substrate to produce fumarate while pyruvate dehyrogenase uses a different substrate and produce a different product: this indicates that the different dehydrogenase carry out distinctly different enzymatic reactions although these dehydrogenase belong to the same family having a common structural domain and sequence homology. on dehydrogenase (i.e. The specific activity of the instant SEQ ID NO: 2 is toward palmitoyl-CoA, with some activity also with stearoyl-CoA substrate. However, the instant specification does not teach that the instant SEQ ID NO: 2 has dehydrogenase activity with palmitoyl-CoA or stearoyl-CoA.

Applicant also argues that the specification at Tables 1-2 (pages 86-90) teach that the nucleic acid encoding the claimed dehydrogenase is differentially expressed in various tumors, therefore the product is good target for cancer therapy.

However, Zhang et al., (IDA) teach that Northern blot analysis showed a transcript of ~2.6 kb of ACAD-9 ubiquitously expressed in most normal tissues with high expression in heart, skeletal muscles, brain, kidney, and liver.

As stated in the previous Office action, the specification fails to teach what kind(s) enzymatic reaction the protein carries out. In other words, the specification fails to teach the substrate of the instant SEQ ID NO: 2 as taught by the post-filing publication of Zhang et al. Voet et al (1990, Biochemistry, John Wiley & Sons, page 507) teach that there are numerous dehydrogenases, each working on a specific substrate and generating a specific product, for example succinate dehyrogenase uses succinate as its substrate to produce fumarate while pyruvate dehyrogenase uses a different substrate and produce a different product: this indicates that the different dehydrogenase carry out distinctly different enzymatic reactions although these dehydrogenase belong to the same family having a common structural domain and sequence homology. Further, the art generally acknowledges that function cannot be predicted based solely on structural similarity to a protein found in the sequence databases. Scott et al (Nature Genetics, 1999, 21:440-443) teach that the function of newly identified gene products is unpredictable even when the database searches reveal significant homology to proteins of known function. Scott et al teaches that the gene causing Pendred syndrome encodes a putative transmembrane protein designated pendrin. Based on sequence similarity data, the authors postulated that the putative protein was deemed to be a member of sulfate transport proteins that included a 29% identity to rat sulfate-anion transporter, 32% similarity to human diastrophic dysplasia sulfate transporter, and 45% similarity to the human sulfate transporter 'downregulated in adenoma'. However, upon analyzing the expression and kinetics of the protein, the data revealed no evidence of sulfate transport wherein results revealed

that pendrin functioned as a transporter of chloride and iodide. Scott et al. states that these results underscore the importance of confirming the function of newly identified gene products even when the database searches reveal significant homology to proteins of known function (page 411, 1st column, 4th paragraph). Skolnick et al. (2000, Trends in Biotech. 18:34-39) state that knowing the protein structure by itself is insufficient to annotate a number of functional classes, and is also insufficient for annotating the specific details of protein function (see Box 2, p. 36). Similarly, Bork (2000, Genome Research 10:398-400) states that the error rate of functional annotations in the sequence database is considerable, making it even more difficult to infer correct function from a structural comparison of a new sequence with a sequence database (see especially p. 399). Such concerns are also echoed by Doerks et al. (1998, Trends in Genetics 14:248-250) who state that (1) functional information is only partially annotated in the database, ignoring multi functionality, resulting in underpredictions of functionality of a new protein and (2) overpredictions of functionality occur because structural similarity often does not necessarily coincide with functional similarity. Smith et al. (1997, Nature Biotechnology 15:1222-1223) remark that there are numerous cases in which proteins having very different functions share structural similarity due to evolution from a common ancestral gene. Brenner (1999, Trends in Genetics 15:132-133) argues that accurate inference of function from homology must be a difficult problem since, assuming there are only about 1000 major gene superfamilies in nature, then most homologs must have different molecular and cellular functions. Bork et al. (1996, Trends in Genetics 12:425-427) add that the software

robots that assign functions to new proteins often assign a function to a whole new protein based on structural similarity of a small domain of the new protein to a small domain of a known protein. Such questionable interpretations are written into the sequence database and are then considered facts. Finally, Bowie et al. (1990, Science 247:1306-1310) state that determination of three dimensional structure from primary amino acid sequence, and the subsequent inference of detailed aspects of function from structure is extremely complex and unlikely to be solved in the near future (p. 1306). Thus, the specification fails to support the asserted credible, specific and substantial utility of the newly identified instantly claimed protein.

Furthermore, the specification does not teach a relationship to any specific disease or establish any involvement SEQ ID NO:2 protein in the etiology of any specific disease. The specification does not teach a relationship between the different tissue distribution of the protein to any specific disease or etiology of any specific disease, either. None of the disorders listed from pages 8-10 is caused by the different distribution of the protein. None of the disorders listed from pages 8-10 is caused by the malfunction of the protein. The specification does not have any substantial use for the antibodies, either. Making and purifying the protein, hybridization probes, antisense, use as query sequence, and the various assays recited in the instant application do not lead to substantial uses of the claimed invention due to unknown functions of the recited protein. Nothing is specific to the sequences of the claimed invention for all of the various probe uses. Any nucleic acid can be used to, identify polymorphisms, map chromosomes, tissue typing, to be used in pharmacogenomic uses, and make

transgenic animals or knockout animals. The specification does not have any substantial use for pharmaceutical compositions, predictive medicine, diagnostic assay, prognostic assays, monitoring effects during clinical trials, and methods of treatment because the specification does not teach what disease(s) is caused by malfunction of the newly discovered SEQ ID NO:2 the protein used in the claimed screening assay. Since EQ ID NO:2 does not have substantial utility, or a well established utility, a compound that binds to SEQ ID NO:2 does not have specific utility, or a well established utility.

As for the second part of the claimed method, i.e. to determine whether the pre-screened SEQ ID NO:2 binding compounds a cytotoxic effect to cancer cells in vitro is not considered to be specific, substantial and credible, for the following reasons: the implicit assertion of anticancer activity for the protein is not substantial. Johnson et al. (Brit. J. Cancer 84(10):1424-1431), in an article entitled "Relationships between drug activity in NCI preclinical in vitro and in vivo models and early clinical trials", state, with regard to the NCI panel that "Agents selected on the basis of potency, selective activity against a particular disease category, and/or differential activity against a few specific cell lines were then evaluated against a small number of sensitive human tumours in the nude mouse xenograft model (citations omitted) as a basis for selecting compounds for further preclinical development. Owing to the large numbers of molecules emerging from the in vitro screen as candidates for xenograft testing, in 1995 this development path was further modified to include a hollow fibre (HF) assay, activity in which was a prerequisite for study in classical xenograft models" (page 1424, second column).

Thus, the initial screen against the 60 cell lines of the NCI panel is not considered by the art to be predictive of *in vivo* activity against tumors, and, as characterized by Johnson et al., such is merely the first of a three-part protocol for identification of agents to be tested in vivo. Further, Shi et al., (J. Chem. Inf. Comput. Sci. 40:367-379), clearly state that "Although cell growth inhibitory activity for a *single* cell line is not very informative, activity *patterns* across the 60 cell lines can provide incisive information on the mechanisms of action of screened compounds...." (abstract). The paper, drawn to methods of mining and visualizing the large amounts of data generated by the NCI panel, further states that relative activity levels distinguish better among the tested cell lines than do the GI_{50} activity patterns, and that "The mean zero preprocessing procedure seemed to eliminate the noninformative "inherent" cytotoxicity, thus brining out the informational differential cell responses (p. 377, end of first column). Thus, Shi et al. indicates that the art does not consider the raw GI_{50} data are insufficient to identify compounds that are likely to be antitumor candidates to be tested further.

In Brenner v. Manson, 148 U.S.P.Q. 689 (Sup. Ct., 1966), a process of producing a novel compound that was structurally analogous to other compounds which were known to possess anti-cancer activity was alleged to be useful because the compound produced thereby was potentially useful as an anti-tumor agent in the absence of evidence supporting this utility. The court expressed the opinion that all chemical compounds are "useful" to the chemical arts when this term is given its broadest interpretation. However, the court held that this broad interpretation was not the intended definition of "useful" as it appears in 35 U.S.C. § 101, which requires that an

invention must have either an **immediately obvious or fully disclosed "real world" utility**. The instant claims are drawn to use of SEQ ID NO:2, which has undetermined function or biological significance. Until some actual and specific activity can be attributed to the SEQ ID NO:2 protein used in the claimed screening assay is incomplete.

Claims 64-72 are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

Conclusion

Any inquiry concerning this communication or earlier communications from the examiner should be directed to MISOOK YU, Ph.D. whose telephone number is 571-272-0839. The examiner can normally be reached on 8 A.M. to 5:30 P.M., every other Friday off.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Jeffrey Siew can be reached on 571-272-0787. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

MISOOK YU, Ph.D.
Primary Examiner
Art Unit 1642